

T. McKelvey

1636

RECEIVED #8

DEC 18 2000

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/540,245A

DATE: 12/06/2000

TIME: 13:00:35

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\12062000\I540245A.raw

ENTERED

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3 <110> APPLICANT: Goodman, Corey
4      Kid, Thomas
5      Brose, Katja
6      Lessier-Lavigne, Marc
8 <120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions
10 <130> FILE REFERENCE: B98-031-3
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/540,245A
C--> 13 <141> CURRENT FILING DATE: 2000-03-31
15 <150> PRIOR APPLICATION NUMBER: 60/065,544
16 <151> PRIOR FILING DATE: 1997-11-14
18 <150> PRIOR APPLICATION NUMBER: 60/081,057
19 <151> PRIOR FILING DATE: 1998-04-07
21 <160> NUMBER OF SEQ ID NOS: 20
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 4758
27 <212> TYPE: DNA
28 <213> ORGANISM: human
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(4758)
34 <400> SEQUENCE: 1
36 atg cgc ggc gtt ggc tgg cag atg ctg tcc ctg tgg ctg ggg tta gtg 48
37 Met Arg Gly Val Gly Trp Glu Met Leu Ser Leu Ser Leu Gly Leu Val
38 1 5 10 15
40 ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc 96
41 Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys
42 20 25 30
44 tct tgc tgc ggc agc aca gtg gac tgt cac ggg ctg gcg ctg cgc agc 144
45 Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser
46 35 40 45
48 gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga 192
49 Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly
50 50 55 60
52 aat aac atc aca aga att acg aca gat ttt gct ggt ctt aga cat 240
53 Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His
54 65 70 75 80
56 cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga 288
57 Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg
58 85 90 95
60 gga qca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga 336
61 Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg
62 100 105 110
64 aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag 384
65 Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys
66 115 120 125
68 cta tac agg ctt gat ctc agt gaa aac caa att cag gca atc cca agg 432

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69 Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg
70      130                      135                      140
72 aaa gct ttc cgt ggg gca gtt gac ata aaa aat ttg caa ctg gat tac 480
73 Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr
74 145                      150                      155                      160
76 aac cag atc agc tgt att gaa gat ggg gca ttc agg gct ctc cgg gac 528
77 Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp
78      165                      170                      175
80 ctg gaa gtg ctc act ctc aac aat aac aac att act aga ctt tct gtg 576
81 Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val
82      180                      185                      190
84 gca agt ttc aac cat atg cct aaa ctt agg act ttt cga ctg cat tca 624
85 Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser
86      195                      200                      205
88 aac aac ctg tat tgt gac tgc cac ctg gcc tgg ctc tcc gac tgg ctt 672
89 Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu
90      210                      215                      220
92 cgc aaa agg cct cgg gtt ggt ctg tac act cag tgt atg ggc ccc tcc 720
93 Arg Lys Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser
94 225                      230                      235                      240
96 cac ctg aga ggc cat aat gta gcc gag gtt caa aaa cga gaa ttt gtc 768
97 His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val
98      245                      250                      255
100 tgc agt gat gag gaa gaa ggt cac cag tca ttt atg gct cct tct tgt 816
101 Cys Ser Asp Glu Glu Glu Gly His Gln Ser Phe Met Ala Pro Ser Cys
102      260                      265                      270
104 agt gtt ttg cac tgc cct gcc gcc tgt acc tgt agc aac aat atc gta 864
105 Ser Val Leu His Cys Pro Ala Ala Cys Thr Cys Ser Asn Asn Ile Val
106      275                      280                      285
108 gac tgt cgt ggg aaa ggt ctc act gag atc ccc aca aat ctt cca gag 912
109 Asp Cys Arg Gly Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu
110      290                      295                      300
112 acc atc aca gaa ata cgt ttg gaa cag aac aca atc aaa gtc atc cct 960
113 Thr Ile Thr Glu Ile Arg Leu Glu Gln Asn Thr Ile Lys Val Ile Pro
114 305                      310                      315                      320
116 cct gga gct ttc tca cca tat aaa aag ctt aga cga att gac ctg agc 1008
117 Pro Gly Ala Phe Ser Pro Tyr Lys Lys Leu Arg Arg Ile Asp Leu Ser
118      325                      330                      335
120 aat aat cag atc tct gaa ctt gca cca gat gct ttc caa gga cta cgc 1056
121 Asn Asn Gln Ile Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg
122      340                      345                      350
124 tct ctg aat tca ctt gtc ctc tat gga aat aaa atc aca gaa ctc ccc 1104
125 Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro
126      355                      360                      365
128 aaa agt tta ttt gaa gga ctg ttt tcc tta cag ctc cta tta ttg aat 1152
129 Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn
130      370                      375                      380
132 gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac 1200
133 Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His

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134	385		390		395		400	
136	aac	ttg	aac	ctt	ctc	tcc	cta	tat
137	asn	leu	asn	leu	leu	ser	leu	tyr
138								
140	aag	ggg	acc	ttt	tca	cct	ctt	cgg
141	lys	gly	thr	phe	ser	pro	leu	arg
142								
144	cag	aac	ccc	ttt	att	tgt	gac	tgc
145	gln	asn	pro	phe	ile	cys	asp	cys
146								
148	ctc	cat	acc	aac	cgg	att	gag	acc
149	leu	his	thr	asn	pro	ile	glu	thr
150								
152	cgc	cgc	ctg	gca	aac	aaa	aga	att
153	arg	arg	leu	ala	asn	lys	arg	ile
154	465							
156	cgt	tgt	tca	ggt	aca	gaa	gat	tat
157	arg	cys	ser	gly	thr	glu	asp	tyr
158								
160	ttt	gcg	gat	ctg	gct	tgc	cct	qaa
161	phe	ala	asp	leu	ala	cys	pro	glu
162								
164	gta	gat	tgc	tct	aat	caa	aag	ctc
165	val	asp	cys	ser	asn	gln	lys	leu
166								
168	cag	tac	act	gca	gag	ttg	cgt	ctc
169	gln	tyr	thr	ala	glu	leu	arg	leu
170								
172	gaa	gcc	aca	gga	atc	ttt	aag	aaa
173	glu	ala	thr	gly	ile	phe	lys	lys
174	545							
176	ttt	agc	aac	aat	aag	atc	aca	gat
177	phe	ser	asn	asn	lys	ile	thr	asp
178								
180	gca	tct	ggt	gta	aat	gaa	ata	ctt
181	ala	ser	gly	val	asn	glu	ile	leu
182								
184	gtg	cag	cat	aag	atg	ttc	aag	gga
185	val	gln	his	lys	met	phe	lys	gly
186								
188	ttg	aga	agc	aat	cga	ata	acc	tgt
189	leu	arg	ser	asn	arg	ile	thr	cys
190								
192	ctc	agt	tct	gtg	cgt	ttg	ctt	tct
193	leu	ser	ser	val	arg	leu	leu	ser
194	625							
196	gtt	gca	cca	ggg	gca	ttt	gat	act
197	val	ala	pro	gly	ala	phe	asp	thr
198								

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200 ctc ttg gcc aat cct ttt aac tgt aac tgc tac ctg gct tgg ttg gga 2016
201 Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly
202 660 665 670
204 gag tgg ctg aga aag aag aga att gtc acg gga aat cct aga tgt caa 2064
205 Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln
206 675 680 685
208 aaa cca tac ttc ctg aaa gaa ata ccc atc caq gat gtg gcc att cag 2112
209 Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala Ile Gln
210 690 695 700
212 gac ttc act tgt gat gac gga aat gat gac aat agt tgc tcc cca ctt 2160
213 Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu
214 705 710 715 720
216 tct cgc tgt cct act gaa tgt act tgc ttg gat aca gtc gtc cga tgt 2208
217 Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys
218 725 730 735
220 agc aac aag ggt ttg aag gtc ttg ccg aaa ggt att cca aga gat gtc 2256
221 Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val
222 740 745 750
224 aca gag ttg tat ctg gat gga aac caa ttt aca ctg gtt ccc aag gaa 2304
225 Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu
226 755 760 765
228 ctc tcc aac tac aaa cat tta aca ctt ata gac tta agt aac aac aga 2352
229 Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg
230 770 775 780
232 ata agc acg ctt tct aat cag agc ttc agc aac atg acc cag ctc ctc 2400
233 Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu
234 785 790 795 800
236 acc tta att ctt agt tac aac cgt ctg aga tgt att cct cct cgc acc 2448
237 Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr
238 805 810 815
240 ttt gat gga tta aag tct ctt cga tta ctt tct cta cat gga aat gac 2496
241 Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp
242 820 825 830
244 att tct gtt gtg cct gaa ggt gct ttc aat gat ctt tct gca tta tca 2544
245 Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser
246 835 840 845
248 cat cta gca att gga gcc aac cct ctt tac tgt gat tgt aac atg cag 2592
249 His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln
250 850 855 860
252 tgg tta tcc gac tgg gtg aag tgc gaa tat aag gag cct gga att gct 2640
253 Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala
254 865 870 875 880
256 cgt tgt gct ggt cct gga gaa atg gca gat aaa ctt tta ctc aca act 2688
257 Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr
258 885 890 895
260 ccc tcc aaa aaa ttt acc tgt caa ggt cct gtg gat gtc aat att cta 2736
261 Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu
262 900 905 910
264 gct aag tgt aac ccc tgc cta tca aat ccg tgt aaa aat gat ggc aca 2784

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265 Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr
266          915          920          925
268 tgt aat agt gat cca gtt gac ttt tac cga tgc acc tgt cca tat ggt 2832
269 Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly
270          930          935          940
272 ttc aag ggg cag gac tgt gat gtc cca att cat gcc tgc atc agt aac 2880
273 Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn
274 945          950          955          960
276 cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat 2928
277 Pro Cys Lys His Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp
278          965          970          975
280 gga ttc tgg tgt att tgt gct gat gga ttt gaa gga gaa aat tgt gaa 2976
281 Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu
282          980          985          990
284 gtc aac gtt gat gat tgt gaa gat aat gac tgt gaa aat aat tct aca 3024
285 Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr
286          995          1000          1005
288 tgt gtc gat ggc att aat aac tac aca tgc ctt tgc cca cct gag tat 3072
289 Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr
290          1010          1015          1020
292 aca ggt gag ttg tgt gag gag aag ctg gac ttc tgt gcc cag gac ctg 3120
293 Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu
294 1025          1030          1035          1040
296 aac ccc tgc cag cac gat tca aag tgc atc cta act cca aag gga ttc 3168
297 Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe
298          1045          1050          1055
300 aaa tgt gac tgc aca cca ggg tac gta ggt gaa cac tgc gac atc gat 3216
301 Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp
302          1060          1065          1070
304 ttt gac gac tgc caa gac aac aag tgt aaa aac gga gcc cac tgc aca 3264
305 Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr
306          1075          1080          1085
308 gat gca gtg aac ggc tat acg tgc ata tgc ccc gaa ggt tac agt ggc 3312
309 Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly
310          1090          1095          1100
312 ttg ttc tgt gag ttt tct cca ccc atg gtc ctc cct cgt acc agc ccc 3360
313 Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Pro Arg Thr Ser Pro
314 1105          1110          1115          1120
316 tgt gat aat ttt gat tgt cag aat gga gct cag tgt atc gtc aga ata 3408
317 Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile
318          1125          1130          1135
320 aat gag cca ata tgt cag tgt ttg cct ggc tat cag gga gaa aag tgt 3456
321 Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys
322          1140          1145          1150
324 gaa aaa ttg gtt agt gtg aat ttt ata aac aaa gag tct tat ctt cag 3504
325 Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln
326          1155          1160          1165
328 att cct tca gcc aag gtt cgg cct cag acg aac ata aca ctt cag att 3552
329 Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile

```

FBI!

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:1152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1179 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:2306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:2320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19